

P. Nolan

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P#21

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/141,220C

DATE: 01/19/2001

TIME: 14:48:27

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3 <110> APPLICANT: Bannon, Gary A
4     Burks, A Wesley
5     Sampson, Hugh
6     Sosin, Howard
8 <120> TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reaction
9     to Allergy
11 <130> FILE REFERENCE: HS102
13 <140> CURRENT APPLICATION NUMBER: 09/141,220C
14 <141> CURRENT FILING DATE: 1998-08-27
16 <150> PRIOR APPLICATION NUMBER: PCT/US96/15222
17 <151> PRIOR FILING DATE: 1996-09-23
19 <150> PRIOR APPLICATION NUMBER: 60/074590
20 <151> PRIOR FILING DATE: 1998-02-13
22 <150> PRIOR APPLICATION NUMBER: 60/074624
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25 <150> PRIOR APPLICATION NUMBER: 60/074633
26 <151> PRIOR FILING DATE: 1998-02-13
28 <160> NUMBER OF SEQ ID NOS: 6
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33 <211> LENGTH: 1930
34 <212> TYPE: DNA
35 <213> ORGANISM: Peanut
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40 tgccaagtca tcaccttacc agaagaaaac agagaacccc tgcgccaga ggtgcctcca 180
41 gagttgtcaa caggaacggg atgaacttgaa gcaaaaggca tgcgagtcct gctgcaccaa 240
42 gctcgagtat gatcctcggt gtgtctatga tcctcgagga cacactggca ccaccaacca 300
43 acgttccctt ccaggggagc ggacacgtgg ccgccaaccc ggagactacg atgatgaccg 360
44 ccgtcaaccc cgaagagagg aaggaggccg atggggacca gctggaccga yggagcgtga 420
45 aagagaagaa gactggagac aaccaagaga agattggagg cgaccaagtc atcagcagcc 480
46 acggaaaata aggccgaag gaagagaagg agaacaagag tggggaacac caggtagcca 540
47 tgtgagggaa gaaacatctc ggaacaaccc ttctacttcc ccgtcaaggc ggtttagcac 600
48 ccgctacggg aacccaaacg gtaggatccg ggtcctgcag aggtttgacc aaaggteaag 660
49 gcagtttccg aatctccaga atcaccttat tgtgcagatc gaggccaaac ctaacactct 720
50 tgttcttccc aagcacgctg atgctgataa catccttgtt atccagcaag ggcaagccac 780
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54 gagcagccga gaccaatcat cctacttgca gggcttcagc aggaatacgt tggaggccgc 1020
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57 gatagtcaaa gtgtcaaaag agcacgttga agaacttact aagcacgcta aatccgtctc 1200
58 aaagaaaygc tccgaagaag agggagatat caccaaccca atcaacttga gagaaggcga 1260
59 gcccgatctt tctaacaact ttgggaagtt atttgaggtg aagccagaca agaagaaccc 1320
60 ccagcttcag gacctggaca tgatgctcac ctgtgtagag atcaaagaag gagctttgat 1380
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61 gctcccacac ttcaactcaa aggccatggt tatcgtcgtc gtcacacaaag gaactggaaa 1440
62 ccttgaactc gtggctgttaa gaaaagagca acaacagagg ggacggcggg aagaagagga 1500
63 ggacgaagac gaagaagagg agggaaagtaa cagagaggtg cgtagggtaca cagcgaggtt 1560
64 gaaggaaggg gatgtgttca tcatgccagc agctcatcca gtagccatca acgcttccctc 1620
65 cgaactccat ctgcttgggt tcggtatcaa cgtcgaatac aaccacagaa tcttccctgc 1680
66 aggtgataag gacaatgtga tagaccagat agagaagcaa gcgaaggatt tagcattccc 1740
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68 tgctcgtcct caatctcaat ctcaatctcc gtcgtctcct gagaaagagt ctctgagaa 1860
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176 <223> OTHER INFORMATION: peptide 20
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181 <223> OTHER INFORMATION: peptide 21

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190 <222> LOCATION: (597)..(606)
191 <223> OTHER INFORMATION: peptide 23
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197 Leu Ala Ser Val Ser Ala Thr His Ala Lys Ser Ser Pro Tyr Gln Lys
198 20 25 30
200 Lys Thr Glu Asn Pro Cys Ala Gln Arg Cys Leu Gln Ser Cys Gln Gln
201 35 40 45
203 Glu Pro Asp Asp Leu Lys Gln Lys Ala Cys Glu Ser Arg Cys Thr Lys
204 50 55 60
206 Leu Glu Tyr Asp Pro Arg Leu Val Tyr Asp Pro Arg Gly His Thr Gly
207 65 70 75 80
209 Thr Thr Asn Gln Arg Ser Pro Pro Gly Glu Arg Thr Arg Gly Arg Gln
210 85 90 95
212 Pro Gly Asp Tyr Asp Asp Asp Arg Arg Gln Pro Arg Arg Glu Glu Gly
213 100 105 110
215 Gly Arg Trp Gly Pro Ala Gly Pro Arg Glu Arg Glu Glu Asp
216 115 120 125
218 Trp Arg Gln Pro Arg Glu Asp Trp Arg Arg Pro Ser His Gln Gln Pro
219 130 135 140
221 Arg Lys Ile Arg Pro Glu Gly Arg Glu Gly Glu Gln Glu Trp Gly Thr
222 145 150 155 160
224 Pro Gly Ser His Val Arg Glu Glu Thr Ser Arg Asn Asn Pro Phe Tyr
225 165 170 175
227 Phe Pro Ser Arg Arg Phe Ser Thr Arg Tyr Gly Asn Gln Asn Gly Arg
228 180 185 190
230 Ile Arg Val Leu Gln Arg Phe Asp Gln Arg Ser Arg Gln Phe Gln Asn
231 195 200 205
233 Leu Gln Asn His Arg Ile Val Gln Ile Glu Ala Lys Pro Asn Thr Leu
234 210 215 220
236 Val Leu Pro Lys His Ala Asp Ala Asp Asn Ile Leu Val Ile Gln Gln
237 225 230 235 240
239 Gly Gln Ala Thr Val Thr Val Ala Asn Gly Asn Asn Arg Lys Ser Phe
240 245 250 255
242 Asn Leu Asp Glu Gly His Ala Leu Arg Ile Pro Ser Gly Phe Ile Ser
243 260 265 270
245 Tyr Ile Leu Asn Arg His Asp Asn Gln Asn Leu Arg Val Ala Lys Ile
246 275 280 285
248 Ser Met Pro Val Asn Thr Pro Gly Gln Phe Glu Asp Phe Phe Pro Ala
249 290 295 300
251 Ser Ser Arg Asp Gln Ser Ser Tyr Leu Gln Glu Phe Ser Arg Asn Thr
252 305 310 315 320

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254 Leu Glu Ala Ala Phe Asn Ala Glu Phe Asn Glu Ile Arg Arg Val Leu
255                      325                      330                      335
257 Leu Glu Glu Asn Ala Gly Gly Glu Gln Glu Glu Arg Gly Gln Arg Arg
258                      340                      345                      350
260 Trp Ser Thr Arg Ser Ser Glu Asn Asn Glu Gly Val Ile Val Lys Val
261                      355                      360                      365
263 Ser Lys Glu His Val Glu Glu Leu Thr Lys His Ala Lys Ser Val Ser
264                      370                      375                      380
266 Lys Lys Gly Ser Glu Glu Glu Gly Asp Tle Thr Asn Pro Ile Asn Leu
267 385                      390                      395                      400
269 Arg Glu Gly Glu Pro Asp Leu Ser Asn Asn Phe Gly Lys Leu Phe Glu
270                      405                      410                      415
272 Val Lys Pro Asp Lys Lys Asn Pro Gln Leu Gln Asp Leu Asp Met Met
273                      420                      425                      430
275 Leu Thr Cys Val Glu Ile Lys Glu Gly Ala Leu Met Leu Pro His Phe
276                      435                      440                      445
278 Asn Ser Lys Ala Met Val Ile Val Val Val Asn Lys Gly Thr Gly Asn
279                      450                      455                      460
281 Leu Glu Leu Val Ala Val Arg Lys Glu Gln Gln Gln Arg Gly Arg Arg
282 465                      470                      475                      480
284 Glu Glu Glu Glu Asp Glu Asp Glu Glu Glu Gly Ser Asn Arg Glu
285                      485                      490                      495
287 Val Arg Arg Tyr Thr Ala Arg Leu Lys Glu Gly Asp Val Phe Ile Met
288                      500                      505                      510
290 Pro Ala Ala His Pro Val Ala Tle Asn Ala Ser Ser Glu Leu His Leu
291                      515                      520                      525
293 Leu Gly Phe Gly Tle Asn Ala Glu Asn Asn His Arg Ile Phe Leu Ala
294                      530                      535                      540
296 Gly Asp Lys Asp Asn Val Ile Asp Gln Ile Glu Lys Gln Ala Lys Asp
297 545                      550                      555                      560
299 Leu Ala Phe Pro Gly Ser Gly Glu Gln Val Glu Lys Leu Ile Lys Asn
300                      565                      570                      575
302 Gln Lys Glu Ser His Phe Val Ser Ala Arg Pro Gln Ser Gln Ser Gln
303                      580                      585                      590
305 Ser Pro Ser Ser Pro Glu Lys Glu Ser Pro Glu Lys Glu Asp Gln Glu
306                      595                      600                      605
308 Glu Glu Asn Gln Gly Gly Lys Gly Pro Leu Leu Ser Tle Leu Lys Ala
309                      610                      615                      620
311 Phe Asn
312 625

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315 <210> SEQ ID NO: 3

316 <211> LENGTH: 474

317 <212> TYPE: DNA

318 <213> ORGANISM: Peanut.

320 <400> SEQUENCE: 3

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323 ccctgcgagc aacatctcat gcagaagatc caacgtgacg aggattcata tgaacgggac 180
324 ccgtacagcc ctagtcagga tccgtacagc cctagtccat atgattcgag aggcgctyga 240

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